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SEQUENCE LISTING

09/674716

<110> BONNEFOY, ^{PATENTS} Yves M.P.
CROWE, James S.
ELLIS, Jonathan H.
RAPSON, Nicholas T.
SHEARIN, Jean

<120> Antibodies to CD23, derivatives thereof, and their therapeutic uses

<130> 1430-256 / PG3433USW0

<140> US 09/674,716

<141> 2001-01-22

<150> CA 2,328,606

<151> 1999-05-07

<150> PCT/GB99/01434

<151> 1999-05-07

<150> GB 9809839.5

<151> 1998-05-09

<160> 54

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ctg att ttt ttt att gtt ctt tta aaa ggg gtc cag agt gaa gtg aag 95
Leu Ile Phe Phe Ile Val Leu Leu Lys Gly Val Gln Ser Glu Val Lys
20 25 30

ctt gag gag tct gga gga ggc ttg gtg caa cct gga gga tcc atg aaa 143
Leu Glu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys
35 40 45

ctc tcc tgt gta gcc tct gga ttt act ttc agt ggc tac tgg atg tct 191
Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Gly Tyr Trp Met Ser
50 55 60

tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg gtt gct gaa att 239
Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile
65 70 75

aga ttg aaa tct gat aat tat gca aca cat tat gcg gag tct gtg aaa	287
Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser Val Lys	
80 85 90 95	
ggg aag ttc acc atc tca aga gat gat tcc aaa agt cgt ctc tac ctg	335
Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg Leu Tyr Leu	
100 105 110	
caa atg aac agc tta aga gct gaa gac agt gga gtt tat tac tgt aca	383
Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Gly Val Tyr Tyr Cys Thr	
115 120 125	
gat ttc ata gac tgg ggc caa ggg aca cta gt	415
Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu	
130 135	
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1 5 10 15	
gtt cag ttt ctg ggg gtg ctt atg ttc tgg atc tct gga gtc agt ggg	95
Val Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser Gly Val Ser Gly	
20 25 30	
gat att gtg ata acc cag gat gaa ctc tcc aat cct gtc act tct gga	143
Asp Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro Val Thr Ser Gly	
35 40 45	
gaa tca gtt tcc atc tcc tgc agg tct agt aag agt ctc ctg tat aag	191
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys	
50 55 60	
gat ggg aag aca tac ttg aat tgg ttt ctg cag aga cca gga caa tct	239
Asp Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser	
65 70 75	
cct cag ctc ctg atg tat ttg atg tcc acc cgt gca tca gga gtc tca	287
Pro Gln Leu Leu Met Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser	
80 85 90 95	
gac cgg ttt agt ggc agt ggg tca ggc aca gat ttc acc ctg gaa atc	335
Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile	
100 105 110	
agt aga gtg aag gct gag gat gtg ggt gtg tat tac tgt caa caa ctt	383

Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
 115 120 125

gta gag tat cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aaa 431
 Val Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
 130 135 140

cgt acg 437
 Arg Thr
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 Leu Met Ser Thr Arg Ala Ser
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 Gln Gln Leu Val Glu Tyr Pro Phe Thr
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 Gly Tyr Trp Met Ser
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 Gly Tyr Trp Met Ser
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 Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser
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Val Lys Gly

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Glu	Ile	Arg	Leu	Lys	Ser	Asp	Asn	Tyr	Ala	Thr	His	Tyr	Ala	Glu	Ser	
1					5				10				15			

gtg aag ggg

Val Lys Gly

57

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Phe Ile Asp

1

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<211> 9

<212> DNA

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<221> CDS

<222> (1)..(9)

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Phe Ile Asp

1

9

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<211> 19

<212> PRT

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<223> Description of Artificial Sequence: Synthetic sequence

<400> 15

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
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Val His Ser

<210> 16

<211> 19
 <212> PRT
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<400> 16
 Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
 1 5 10 15

Ala Gln Ala

<210> 17
 <211> 348
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 region

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 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15

gag ccg gcc tcc atc tcc tgt cgc tcg agt aag agt ctc ctg tat aag 96
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
 20 25 30

gat ggg aag aca tac ttg aat tgg tac ctg cag aag cca ggg cag tct 144
 Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

cca cag ctc ctg atc tat ttg atg tcc acc cgg gca tca ggg gtc cct 192
 Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro
 50 55 60

gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc 240
 Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

agc aga gtg gag gct gag gat gtt ggg gtt tat tac tgtcaa cag ctg 288
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
 85 90 95

gta gag tat cca ttc acg ttc ggc caa ggg acc aag gtg gag atc aaa 336
 Val Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

cgt acg gtg gct 348

Arg Thr Val Ala
115

<210> 18

<211> 1335

<212> DNA

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<220>

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Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly	
1			5							10			15			

tcc	ctt	aga	ctc	tcc	tgt	gca	gct	agc	gga	ttc	act	ttc	agt	ggc	tac	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Gly	Tyr	
20			25								30					

tgg	atg	tcc	tgg	gtc	cgc	cag	gct	cca	ggg	aag	ggg	ctc	gag	tgg	gtt	144
Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
35			40							45						

gct	gaa	att	aga	ttg	aaa	tct	gat	aat	tat	gca	aca	cat	tat	gcg	gag	192
Ala	Glu	Ile	Arg	Leu	Lys	Ser	Asp	Asn	Tyr	Ala	Thr	His	Tyr	Ala	Glu	
50			55							60						

tct	gtg	aag	ggg	aaa	ttc	acc	atc	tca	aga	gat	gat	tca	aaa	tct	aga	240
Ser	Val	Lys	Gly	Lys	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Arg	
65			70				75			80						

ctg	tat	ctg	caa	atg	aac	agc	ctg	aaa	acc	gag	gac	aca	gcc	gtg	tat	288
Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr	
85			90						95							

tac	tgt	aca	gat	ttc	ata	gac	tgg	ggc	cag	gga	aca	cta	gtc	acc	gtc	336
Tyr	Cys	Thr	Asp	Phe	Ile	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
100			105				110									

tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	384
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
115			120				125									

tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	432
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
130			135				140									

gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	480
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
145			150				155			160						

acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc	528
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
165 170 175	
tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc	576
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr	
180 185 190	
cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg	624
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
195 200 205	
gac aag aaa gtg gag ccc aaa tct tgt gac aaa act cac aca tgc cca	672
Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro	
210 215 220	
ccg tgc cca gca cct gaa ctc gcg ggg gca ccg tca gtc ttc ctc ttc	720
Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe	
225 230 235 240	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	768
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
245 250 255	
aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	816
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
260 265 270	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg	864
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
275 280 285	
cg ^g gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc	912
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
290 295 300	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc	960
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
305 310 315 320	
tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc	1008
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	
325 330 335	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg	1056
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
340 345 350	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc	1104
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
355 360 365	
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg	1152
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
370 375 380	
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc	1200

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser				
385	390	395	400	
ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag				1248
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln				
405		410	415	
ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac				1296
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His				
420		425	430	
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga				1335
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys				
435		440		
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<211> 57				
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gatcaagctt ctctacagtt actgagcaca	30
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ggc	63
<210> 25	
<211> 63	
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cgctcgagta agagtctcct gtataaggat gggaaagacat acttgaattt gtacctgcag 60	60
aag	63
<210> 26	
<211> 36	
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tgatgcccggtggacatca aatagatcag gagctg	36
<210> 27	
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ttgatgtcca cccgggcata aggggtccct gacagg 36

<210> 28
<211> 84
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<223> Description of Artificial Sequence: Oligonucleotide

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agccaccta cgtttgcata ccacccgtt cccttggccg aacgtgaatg gataactctac 60
cagctgttga cagtaataaa cccc 84

<210> 29
<211> 60
<212> DNA
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<223> Description of Artificial Sequence: Oligonucleotide

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<210> 30
<211> 66
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cgccat 66

<210> 31
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gacaca 66

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ctcggttt 69

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<211> 48
<212> DNA
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<400> 37

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aagcttccgt cgaattcatt tacccggaga cag	33
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actagtcgac atgaagtttc cttctcaact tctgctc	37
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Thr Lys Leu Glu Ile Lys Arg Thr
 1 5

<210> 43
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<220>
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<400> 43
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 1 5

<210> 44
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<400> 44
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 1 5

<210> 45
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 aacttccctt tcacagactc cgcataatgt gttgcataat tatcagattt caatctaatt 180
 tcagcaaccc actcaagccc cttctctgga gactggcgga cccaaagacat ccagtagcca 240
 ctgaaagtaa atccagaggc tacacaggag agtttcatgg atcctccagg ttgcaccaag 300
 cctcctccag actcctcaag cttcacttca ctctggaccc cttttaaaag aacaataaaa 360
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 tggcctgac ccactgcccac taaaccggc tgagactcct gatgcacggg tgacatcaa 180
 atacatcagg agctgaggag attgtctgg tctctgcaga aaccaattca agtatgtctt 240
 cccatccta tacaggagac tcttaactaga cctgcaggag atggaaactg attctccaga 300
 agtgacagga ttggagagtt catcctgggt tatcacaata tccccactga ctccagagat 360
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 gagtaactgt aaagctt 437

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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Humanised anti-CD23 antibody VL region

<400> 48
 agccaccgta cgtttcatct ccacccgggt cccttggccg aacgtgaatg gatactctac 60
 cagctgtga cagtaataaa ccccaacatc ctcagccctcc actctgctga ttttcaagtgt 120
 aaaatctgtg cctgatccac tgccactgaa cctgtcaggg acccctgatg cccgggtgg 180
 catcaaatacg atcaggagct gtggagactg ccctggcttc tgcaggtacc aattcaagta 240
 tgtcttccca tccttataca ggagactctt actcgagcga caggagatgg aggccggctc 300
 tccagggggtg acggcaggag agagtggaga ctgagtcata acaatatac 348

<210> 49
 <211> 1335
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Humanised anti-CD23 antibody VH region

<400> 49
 tcatttaccc ggagacaggg agaggctctt ctgcgtgtag tggttgtca gaggctcatg 60
 catcacggag catgagaaga cgttccctg ctgccacctg ctcttgcata cggtagctt 120
 gctgttagagg aagaaggagc cgtcggagtc cagcacggg ggcgtggct ttagttgtt 180
 ctccggctgc ccattgctct cccactccac ggcgtatgc ctggataga agccttgcac 240
 caggcaggtc aggctgaccc ggttcttggg cagctcatcc cgggatgggg gcagggtgt 300
 cacctgtgtt tctcggggct gccccttggc tttggagatg gttttctcga tgggggtgg 360
 gagggctttt ttggagaccc tgcacttgta ctccctgcca ttcagccagt cctgggtgcag 420
 gacgggtgagg acgctgacca cacggtagt gctgttgc tgcctctccc gcggcttgc 480
 cttggcattt tgcacccca cggccatccac gtaccagttt aacttgaccc cagggtcttc 540
 gtggctcacg tccaccacca cgcattgtac ctcagggtc cgggagatca tgagggtgtc 600
 cttgggtttt gggggaaaga ggaagactga cgggtcccccc gcgagttcag gtgctggca 660
 cggtgggcat gtgtgagtt tgcacaaga tttggctcc actttttgtt ccaccttgg 720
 gttgctggc ttgtgattca cgttgcagat gtaggtctgg gtgcccagc tgctggaggg 780
 cacgggtcacc acgctgctga gggagtagag tcctgaggac tgcggacac cggggaaagg 840
 gtgcacggccg ctggtcaggc cgcctgagtt ccacggacacc gtcaccgggtt cggggaaagta 900
 gtccttgacc aggagccca gggccgtgt gccccccagag gtgctctgg aggagggtgc 960
 cagggggaaag accgatgggc cttgggtgg ggcgtggaggg acgggtgacta gtgttccctg 1020
 gccccagttt atgaaatctg tacagtaata cacggctgtg tcctcggtt tcaggctgtt 1080
 catttgacca tacagtcttag atttgaatc atctttgttgc atggtaatt tccccttcac 1140

agactccgca taatgtgttg cataattatac agatttcaat ctaatttcag caacccactc 1200
 gagcccccttc cctggagcct ggcggaccca ggacatccag tagccactga aagtgaatcc 1260
 gctagctgca caggagagtc taagggaccc cccgggctt accaagcctc ccccagactc 1320
 caccagctgc acctc 1335

<210> 50
 <211> 137
 <212> PRT
 <213> Mus musculus

<400> 50
 Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Asp Phe Gly Leu
 1 5 10 15

Ile Phe Phe Ile Val Leu Leu Lys Gly Val Gln Ser Glu Val Lys Leu
 20 25 30

Glu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu
 35 40 45

Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Gly Tyr Trp Met Ser Trp
 50 55 60

Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg
 65 70 75 80

Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser Val Lys Gly
 85 90 95

Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg Leu Tyr Leu Gln
 100 105 110

Met Asn Ser Leu Arg Ala Glu Asp Ser Gly Val Tyr Tyr Cys Thr Asp
 115 120 125

Phe Ile Asp Trp Gly Gln Gly Thr Leu
 130 135

<210> 51
 <211> 145
 <212> PRT
 <213> Mus musculus

<400> 51
 Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Arg Phe Ser Val
 1 5 10 15

Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser Gly Val Ser Gly Asp
 20 25 30

Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro Val Thr Ser Gly Glu
 35 40 45

Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys Asp
 50 55 60

Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro
 65 70 75 80

Gln Leu Leu Met Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser Asp
 85 90 95

Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile Ser
 100 105 110

Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu Val
 115 120 125

Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
 130 135 140

Thr
 145

<210> 52

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanised anti-CD23 antibody VL
 region

<400> 52

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
 20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
 85 90 95

Val Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

Arg Thr Val Ala
 115

<210> 53

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanised anti-CD23 antibody VH region

<400> 53

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly
1				5						10				15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Gly	Tyr
								20		25			30		

Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
								35		40			45		

Ala	Glu	Ile	Arg	Leu	Lys	Ser	Asp	Asn	Tyr	Ala	Thr	His	Tyr	Ala	Glu
								50		55		60			

Ser	Val	Lys	Gly	Lys	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Arg
							65		70		75		80		

Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr
								85		90		95			

Tyr	Cys	Thr	Asp	Phe	Ile	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
								100		105		110			

Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser
								115		120		125			

Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys
								130		135		140			

Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu
								145		150		155		160	

Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu
								165		170		175			

Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr
								180		185		190			

Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val
								195		200		205			

Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro
								210		215		220			

Pro	Cys	Pro	Ala	Pro	Glu	Leu	Ala	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe
								225		230		235		240	

Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
								245		250		255			

Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
								260		265		270			

Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
275						280						285			
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
290						295						300			
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
305						310				315					320
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
									330					335	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg
									345					350	
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
								360				365			
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
									375				380		
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
									390			395			400
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln
									405			410			415
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
									420			425			430
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
									435			440			
<210> 54															
<211> 8															
<212> PRT															
<213> Homo sapiens															
<400> 54															
His Ser Ile Gly Lys Val Ile Ile															
1 5															